

FIG. 1

Consensus	90
BDV JCT	90
BDV Briese	90
GTTGGTTAAACAACCAACATCATATATCTTCTARCAAAATGAACACACGCAATGCCACCAAGAGAGCGCTGTTGATGACGCCGATGA...T.C.....C...C.T.....	
Consensus	180
BDV JCT	180
BDV Briese	180
CCATGGAGGAYCAAGATYTATATGAACCCCGAGCGCTCCCYAAGCTCCCYGGRPAATTCCTACAATACACCGTTGGGGGGTCTGACCC.....T.....T.....C.....T.....T.G.....	
Consensus	270
BDV JCT	270
BDV Briese	270
CGCATCGGGTATAGGCATGAGAARGATCAGGCAGAACCGCAGTGGCATTTGAGCACATCAGCGCGCATATGTTTCAYACAGTAAG.T.....T.....A.C.....C.....	
Consensus	360
BDV JCT	360
BDV Briese	360
CGCCYAGCCTTGTTCTATGTTGCTAATCCCGAGACTGCACGCTGCGTTTGTTCACGGAGGGTGCCTCGTGAATCTTACCTGTGCGAC.....T.....T.....C.....	
Consensus	450
BDV JCT	450
BDV Briese	450
CGCCTGTACGCGTGGGAACAGACTGTGTAAAGACTGCRAAGTTTACGGGGAAAGACRACRACGCGTGATCTCACCGAGCTGGAGAT.....C.....A.....G.....A.....C.....T.....G.....	
Consensus	540
BDV JCT	540
BDV Briese	540
TCTCCTCTATMTTCAGCCATGTTGCTCATTACTAATWGGGTTGTGATAGGATCGTCTCTAAGATYAAGCAGGAGCCGAGCAGATCAA.....T.....C.....A.....G.....C.....	
Consensus	630
BDV JCT	630
BDV Briese	630
AGAAAAGGTTTAAACTATGATGGCAGCCTTAAACCGGCCATCCCATGGTGAGACTGTACACTACTYACAGATGTTTAAATCCACATGAGGT.....T.....C.....	

FIG. 2A

Consensus	CTATAGATTGGATTAAAGCCARCCCTGGGTAGGCTCCTTTTGTGTCTCTACTAACTACAGACTTTGAGTCCCCAGGTAAGAATTYYA	720
BDV JCTG.....	720
BDV BrieseA.....T.	720
Consensus	TGGAYCAGATTAACTTTGTCGCAAGTTATGRCAGATGACTACGTACACTACTATAAAGGAGTACCTGCAGAAATGYATGGATGCTACCC	810
BDV JCTA.....G.....T.....	810
BDV BrieseG.....A.....C.....	810
Consensus	TTACAATCCCYGTAGTTGCATATGAGATYCGTGACTTTTGAAGTTTCAGCAAGCTTAARGAGGAWCATGCTGACCTGTTTCCGTTTC	900
BDV JCTT.....T.....C.....T.....A.....T.....C.....	900
BDV BrieseC.....C.....G.....T.....C.....	900
Consensus	TGGGGCYATTMGRCAACCCCGCGCTATCAAGCTKGGCCGACGACGCTTTCCCAATCTGGCYTCYGCAGCGTTTACTGGAGTAAGAAG	990
BDV JCTT.....C.....G.....T.....G.....T.....C.....	990
BDV BrieseC.....A.....G.....A.....C.....	990
Consensus	ARAAYCCCAATGGCRGGCTACCGGCGCTCCACCATCCAGCGGCGCRAGTGTCAAGGARACCCAGCTTGCCCGGTATAGCGCGCGCG	1080
BDV JCTG.....T.....G.....G.....G.....	1080
BDV BrieseA.....A.....A.....A.....A.....	1080
Consensus	AGATATCTCGYGGRGARGACGGGGCAGAGCTCTCAGTGAGATCTCTGCCATATGARRATAGTAGTGTGACTGGTCTAACTARAAA	1170
BDV JCTC.....G.....A.....G.....G.....	1170
BDV BrieseT.....A.....G.....A.....AG.....A.....	1170
Consensus	CAATGAACAAACCAATAAAAAACCAATGCGGCAACCCYCCGACCTGYGATGAGTCCGACCTCCCGCTGACATTTGCTTGAATAGT	1260
BDV JCTC.....C.....T.....T.....T.....T.....	1260
BDV BrieseT.....C.....C.....C.....C.....	1260
Consensus	CAGGAGGCTCAATGGCAACGSGACCCATCGAGTCTGTGTCGACTCCCTGGAGACGAAGAAGATCCCCAGACACTACGACGGGAACGAYCGS	1350
BDV JCTG.....C.....T.....	1350
BDV BrieseC.....C.....C.....	1350

FIG. 2B

Consensus	GGTCACCAAGACACCGGAAGRTCCCAAGGAATGCATTGACCCCAACCRGTAGACCACTCCTGAGGACCTCAGGAAGAACCCTCCATGA	1440
BDV JCTA.....G.....A.....	1440
BDV BrieseG.....A.....	1440
Consensus	TCTCAGACCCAGACGACCGAACCAGGAGGAGCTCTCGAATGATGAGCTWATCAAGAAGYTAGTGACGGAGCTGGCCGAGAAATAGCA	1530
BDV JCTA.....G.....T.....C.....	1530
BDV BrieseG.....A.....T.....	1530
Consensus	TGATCGAGGTGAGGAGGTCCGGGCACTCTTTGGRGACATCTCGGCTCGYATCGAGGAGGTTTGAGTCCCTGTCCGCCCTCCCAAGTGG	1620
BDV JCTG.....A.....C.....T.....	1620
BDV BrieseA.....T.....	1620
Consensus	AAACCATCCAGACAGCTCAGCGGTGCGAYCACCTCGAYAGCATCAGRATCCTYGGCGAGAACATCAAGATACTRGATCGCTCCATGAAGA	1710
BDV JCTC.....T.....A.....T.....G.....	1710
BDV BrieseT.....C.....G.....C.....A.....	1710
Consensus	CAATGATGGAGACAAATGAAGCTCATGATGGAGAAGGTGGAYCTCCTTACGATCAACCCCGTGGGACCTCTGCACCCATGTTGGCCT	1800
BDV JCTC.....T.....	1800
BDV BrieseG.....	1800
Consensus	CCCATCCTGCACCTCCGGCATTTATCCCAAGCTCCCAAGTGCCCGACARCGGATGARTGGGACATCATACCATATAAAATCGAATCA	1890
BDV JCTG.....A.....	1890
BDV BrieseA.....	1890
Consensus	CCATGAATTCAAARCATTCCTATGTGGAGCTCAAGGRCAAGTAATCGTCCCTGGATGGCCACACTGATGCTTGAGATAGACTTTGTAG	1980
BDV JCTG.....A.....	1980
BDV BrieseA.....	1980
Consensus	GRGGGACTTCACGGAACCAAGTTCTCTTAACATCCCATTTCTTTTCAGTGAAGAGACCTCTGCAGCTTCCACGCGAGAGAAGTTGACCCGACT	2070
BDV JCT	.A.....	2070
BDV Briese	.G.....	2070

FIG. 2C

Consensus	ACTTYACYATTGAGTAGARCCAGGTCATTCCTGGTCAAYATATATCTCCAGATTGACGACTCTCTGGTCTCTAACACTCACTCAC	2160
BDV JCT	...C.C.....G.....C.....T.....	2160
BDV Briese	...T.T.....A.....T.....	2160
Consensus	TRTCYGTTRTACAGGACCCGATTAGRAAATACATGTTCCACGGCTCACAAGAMCAGAGCAACGCAATYATGACGCTTCAATG	2250
BDV JCT	.G.C.A.....G.....A.....A.....T.....T.....	2250
BDV Briese	.A.T.G.....A.....C.....C.....C.....	2250
Consensus	TCTTYTCTATCGGCTTCGGACATTGGTGTGGYCCTCTCGGGCCCGACATTCGATCTTCAGGGCCTTAGYTGCAATACTGACTCCACT	2340
BDV JCT	...C.....C.....A.....G.....T.....C.....	2340
BDV Briese	...T.....T.....G.....C.....	2340
Consensus	CCTGGAATATGAYCTGGAGATAAGCGACTTTGCCACACCCCAACGGAAATGTCTATTCATGCGAGGTAGTTATCTYAAACACACG	2430
BDV JCT	...T.A.C.T.....T.....T.....T.....	2430
BDV Briese	...C.G.T.C.....C.....C.....	2430
Consensus	ACTATTAGCTCCGGCAGTCCACACACTCATGCCCTCAAGTACCACCTGCAAAACCTATTGGGATTCCTTTGGTAGCTACAGGGCTGACCGA	2520
BDV JCT	...G.....A.....	2520
BDV Briese	...A.....	2520
Consensus	ATCATMAATCGGTACACTGGTACTGTTAAGGTTGTYYTAACTACTACRCAGAGGAYCCCTTCGAGTGCACACTGGTTCTACTGCTGC	2610
BDV JCT	...C.....T.....G.....T.....	2610
BDV Briese	...A.....C.....A.....C.....	2610
Consensus	TCGGCGATTACACAGAGATCTGCCGATGCTCTATTACAAATGTACGGTGGCTGTACARACATTCACCGTTTCATGTACTGCAGTTTY	2700
BDV JCT	...A.....G.....C.....	2700
BDV Briese	...G.....A.....T.....	2700
Consensus	GCRGACTGYAGTACGTGAGYCARCAGGAGCTAGAGAGTGGMAAGGCAATGCTGAGCGATGGCAGTACMTTAACTTATACCCCGTATATC	2790
BDV JCT seq	..G....T....T....G....C....C....	2790
BDV Briese	..A....C....C....C....A....A....A....	2790

FIG. 2D

Consensus	2880
BDV JCT	2880
BDV Briese	2880
YTACARTCAGAGTCTGACAAACCCCTTAATGGGACATCTCTGCAACTCATCTCTCAAGATAGTTCTTCGATGAATTTAGGCGT T...A...T...T...T...C...T... C...G...C...C...C...C...T...	
Consensus	2970
BDV JCT	2970
BDV Briese	2970
TCATATCCCTARCGAATGTAGTTACGAGAGCTCATCAATGACGTGTGAAACTACAGCTCGTCTGCGGCGCCARCTTGARAG.....T.....T.....A.....G.....A.....C.....C.....C.....G.....A.....	
Consensus	3060
BDV JCT	3060
BDV Briese	3060
AGCGCGCTAGGGAYACYCARCAGATTGAGTAYCTAGTTACAGCTTAGGCCYACACTGAAAGATGCTGGGAGGACTGTGAGATCCTCT...A.....C.....T.....G.....C...C..G.....T.....C.....A.....	
Consensus	3150
BDV JCT	3150
BDV Briese	3150
CAGTCTCTGCTCTAGGGRTGTTTGGTACTGGGATYGCAAGTGCTTCKCAATTTTGGAGRGCTGGCTCAACCCACCTGAYATCATCGGGA.....T.....G.....C.....T.....G.....C.....T.....A.....C.....	
Consensus	3240
BDV JCT	3240
BDV Briese	3240
TATATAGTTAATGGAGTTGGGTGTCGCAATGCCATCGTGTAAATGTACGTTTCATGGCTGGAATGAGTCCACMTATTACCTCCAA.....T.....A.....A.....T.....C.....C.....	
Consensus	3330
BDV JCT	3330
BDV Briese	3330
GTAGATTACAATGGRCGGAAGTACTTCTGAATCATGAGGGRAGGYTACAACAACACCCCGAGGCGGCTTAAGCGGCTCA.....T.....G.....C.....G.....C.....A...T.....	
Consensus	3420
BDV JCT	3420
BDV Briese	3420
ATGTGTTGCGCAGGTACTTCCTAGGGACAGTAGGGTCTGGGTGAACCGAGGAGATTCTGGTACAATAAGACCTCATGATACCAT.....T.....T.....C.....T.....C.....C.....	
Consensus	3510
BDV JCT	3510
BDV Briese	3510
CTFGAGGAGTTTGAGGCAAGTCTCAACATGACCCCYCAGACCAGTATCGCTCGGTCTCATGAGACAGACGCCCAATAAATCATGCCTACGGAA.....C.....T.....G.....T.....	

FIG. 2E

Consensus	ACGCAGGTGAYCTCCTTCCATACACAGGTCTAGTAATATAAORTCTACRGATACAGGCTCAGGCTGGGTGCACATCGGCCTACCCCTCA	3600
BDV JCTC.....G.....A.....	3600
BDV BrieseT.....A.....G.....	3600
Consensus	TTTGCTTTCCTCAATCCYCTCGGGTGGCTYAGGGACCTACTTGGTGGCGCTGGTGGGTGGGTTCTATACCTTAATAAGTCTTTGT	3690
BDV JCTT.....G.....G.....	3690
BDV BrieseC.....A.....A.....	3690
Consensus	GTTTCCTTACCAGCCTCCTTCGCGAGGAGAGACGCTCGGCCGGTGGCAGGAATAAACCGTACCACCAACCTCTTAAACCCCTCTYC	3780
BDV JCTAA.....GT.....	3780
BDV BrieseGT.....	3780
Consensus	TCGGRACAGAGGTCTCTTCTGCTTAARTCGAGVTCACCTCCGCCCATCACTGAGCAGCAYTRGGCCAGATTAAAGCAARGAACCTGGCAT	3870
BDV JCTG.....A.....T.....C.....T.G.....A.....	3870
BDV BrieseA.....G.....C.....T.....C.A.....G.....	3870
Consensus	CCTGTGACTATTACTTCCGCCAAGTTGTTATTTGCCCTGAAAGTATATCCCATTTGGTGTYYTAAAGAGCTGCGGAGGCTATAC	3960
BDV JCTG.....CT.....C.....	3960
BDV BrieseTC.....T.....	3960
Consensus	TAACAGTTATAGTATCAGCTTGGAGCTGGATCAATGATGACRAAGACCCCTATATCTCTCTGTGAGATATGCACCTCACCATCCCGGGTCC	4050
BDV JCTC.....A.....G.....	4050
BDV BrieseT.....G.....	4050
Consensus	GRGCCCACTTGAGCTYCACATTGCCTACAGCGCATAGTGGGTGAGTCTCTGTAYAGCCGGGARGCAGATATAGGGCCAAAGGCTTG	4140
BDV JCTC.....T.....A.....T.....	4140
BDV BrieseT.....C.....G.....C.....	4140
Consensus	GGATATGCTATTGCATTCCTCAATCYCTGTTATTGCCACCATAGACACACACACAGCTGCGCTTAATGACCTACACCACTTCTTCTGCTG	4230
BDV JCTC.....A.G.....	4230
BDV BrieseT.....G.A.....	4230

FIG. 2F

Consensus	CAGCAGACACAGCCAGAGCAGATGCCAYCTCCTTAATCGCCTCAGTGGTCCAGRGCCCTTTGGGARCAAGGTCATTCTTGATCATA	4320
BDV JCTC.....A..A.....G.....	4320
BDV BrieseT.....G..G.....A.....	4320
Consensus	TAATCAACATGATCGACAYATTGACTCAATCAACCTCCCCCATGATGATTACTTCAACAATTATTAAAGTCTATCTTCCCTACTCCCAAG	4410
BDV JCTC.....T.....	4410
BDV BrieseT.....T.....T.....	4410
Consensus	GGCTTGTTATGGGAGGCAYAAATGTRTCAAGTCTCCTCTGATTTCGCTCCGATTTTCRYATTCCTGAATYATGCCRCRCAACATGACAGCT	4500
BDV JCTC.....G.....T.....A..T.....C.....A.....	4500
BDV BrieseT.....A.....C.....G..C.....T.....G.....	4500
Consensus	TACTAAAAAACTGCTYCAACTTGACCCYGTTCCTCCTCATGGTCTCTTCGGTGCAGAAAGTCATGGTACTTCCCTCGAGATCCGAATGG	4590
BDV JCTT.....T.....	4590
BDV BrieseC.....C.....	4590
Consensus	TYGACGGGTCACGGGACAGCTCCACAAGATGCGTGTGAGCTGGARACGCCCAAGCCCTGCTGTCRTACGGCCATACCCCTCTGTCAA	4680
BDV JCTT.....G.....A.....	4680
BDV BrieseC.....A.....G.....	4680
Consensus	TATTTGRCAGAGTTTATCAAAAGGCTATGTTCTCAAAGAATGCGAAGTGGCGCCYGTACACCTGCTCCAGGCTGTGACAAATCCATAA	4770
BDV JCTA.....T.....	4770
BDV BrieseG.....C.....	4770
Consensus	ARATGCGAGAGCTGGCGCGCTGGAGCCCGYRTTTGACCGACGATGGCAGCTTTCGMAAGGTTGTCATTCTAAGAATTGCTGACC	4860
BDV JCTG.....TG.....C.....	4860
BDV BrieseA.....CA.....A.....	4860
Consensus	TAGATATGGATCCCGACTTCAACGATATTGTTAGCGAYAAGCGATAATCAGCTCAAGAGGGACTGGGTATTTYGATACAAATGCACRG	4950
BDV JCTC.....	4950
BDV BrieseT.....T.....C.....G.....	4950

FIG. 2G

Consensus	CTTTTGGGAAGAAATACRGCTGARCCTGGAGAGGCCYCTGCCAGTCGGGACCCRTACGRCCTTGTGAATGCTCTCTATCGATGGAGCGCT	5040
BDV JCTA.....G.....C.....A.....A.....G.....G.....G.....	5040
BDV BrieseG.....A.....T.....G.....G.....A.....A.....A.....	5040
Consensus	TAGAYAAATATCCAGCCCTGCTAGACCAATTTTACAGGGAGCGGTTGAGTTYGAGGATCGGYTACTGTCTGCTGCTTAAAGAGAARG	5130
BDV JCTT.....A.....T.....T.....C.....C.....G.....G.....	5130
BDV BrieseC.....C.....C.....C.....T.....T.....A.....A.....	5130
Consensus	AGTTTAAAGGTAAAGGGAAGGTTCTTCTCGAAGCAAAACATTGGCAATCAGGATATATCAGGTTGTGCTGAAGCTGCACCTTAAGAAAYGAGG	5220
BDV JCTG.....A.....T.....C.....T.....C.....T.....	5220
BDV BrieseA.....A.....T.....C.....T.....C.....T.....	5220
Consensus	TTATGCCATACYTAAARACACAYTCAATGACCATGAGCTCAACGGCYTAACYCAVCTTCTTAACCGGCTATCACATCTACTACTAARG	5310
BDV JCTT.....A.....T.....C.....C.....C.....T.....	5310
BDV BrieseC.....G.....C.....C.....T.....T.....C.....	5310
Consensus	GTGACTCCTTTGTATTAAACYTWGAYTATAGYTCCTGCTGCAACGGTTCCGACCAAGAACTRCARGCCCCAMTCTGTCGTCAGTTGGATC	5400
BDV JCTT.A..T.....C.....T.....A.....A.....C.....	5400
BDV BrieseC.T..C.....T.....G.....G.....A.....	5400
Consensus	AGATGTTCAATTCGGGTACTCTTTCAGGACTGGGTGCACACTGCCATGCTTTACACCGTTTATTATTTCARGACAGRTTCAACCCGCCCT	5490
BDV JCTA.....A.....A.....A.....A.....A.....	5490
BDV BrieseA.....A.....A.....A.....A.....A.....	5490
Consensus	ATTCCTCMTGCTGAGCCCGTTGAAGACGGWGYACATGCGCGGTTGGGACTAARACAACTGGGAGGGYATGAGGCAGAAACTATGGA	5580
BDV JCTT..C.....T..C.....T..C.....A.....T.....	5580
BDV BrieseC..A.....A..T.....A.....G.....C.....C.....	5580
Consensus	CAATYCTTACGAGCTGCTGGAGATAATTGCTCTCTCGGGAATTAACGTGACGTTTAAATATAGGCCARGGTGATATCAGACAAATCA	5670
BDV JCTT.....T.....T.....G.....G.....	5670
BDV BrieseC.....C.....C.....C.....A.....A.....	5670

FIG. 2H

Consensus	TYRTACATAATCTGCAAGCCAAATAAAYCAGCTATTAGCGGAGCGAGCAYTRGRCYTYGTACAAAGCATGCTAGATTAGCTGGCCATA	5760
BDV JCT	..TG.....T.....T.G..A..TT.....	5760
BDV Briese	..CA.....C.....C.A..G..CC.....	5760
Consensus	ACCTYAAGGTAGARGNATGYTGGGTGTCAGATTCTCTGTATGAGTATGGAAGAAGCTTCTTCGGTGGGTACCTGTCCCGGGCTGTT	5850
BDV JCT	..T.....A.....T.....C.....A.....	5850
BDV Briese	..C.....G.....C.....T.....T.....G.....	5850
Consensus	TGAAGCAGCTCTCRGGGTGACGGAYTCYACTGGRGAGYTATTCCAAACCTATACTCAAAGTTAGCCTGCTTAAACATCATCTGTGTTAA	5940
BDV JCTG.....C.C.....G..T.....A..C.....	5940
BDV BrieseA.....T..T.....A..C.....G..T.....	5940
Consensus	GCGCAGCGATGCGCAGACACATCYCCATGGGTGGCACTCCGGCAGGTGTCCTCTGTATCTTATCGAGTTRTATGTTGAGCTGCCTCCRG	6030
BDV JCTC.....C.....G.....G.....G.....	6030
BDV BrieseT.....T.....A.....A.....A.....	6030
Consensus	CAATCATGCAGGAYGAGTCGCTRTTRACGACCCCTCTGYCTCGTAGGYCCATCCATTGGTGGGCTTCRACYCCCTGCAACCCCTGCCAGTG	6120
BDV JCTC.....G..A.....T.....T.....A..T.....G.....	6120
BDV BrieseT.....A..G.....C.....C.....G..C.....A.....	6120
Consensus	TCITTTTCAGAGGAATGTCGACCCAYTGCCCTTTCAGCTAGCACTCTTGAGACCCCTCATTAAACGACAGGGTGACYTGTAGCTTGG	6210
BDV JCTT.....C.....A.....A.....T.....	6210
BDV BrieseC.....C.....G.....G.....C.....	6210
Consensus	TGATCGTGTGGTYAAGTTACGGATAGCACCCCTATCCAGACTGGCTCTCYCTAGTGACTACCCGACYTCACCTCAACATTGCYCARGTGT	6300
BDV JCTT.....C.....C.....T.....T.....T..G.....	6300
BDV BrieseC.....T.....T.....C.....C.....A.....	6300
Consensus	ACCGGCCAGAACGTCARATCAGGAGGTGGATTGAGGARGCRATAGCRACAAAGCTCACACTCGTCACGCATAGCAACTTTTTCAGCAGS	6390
BDV JCTA.....G.....G..A.....A.....T.....G.....	6390
BDV BrieseG.....A..G.....G.....C.....C.....C.....	6390

FIG. 2I

Consensus	CCCTCAGGAGATGGCYCAGYTGCTTGGAGGGAGCTTCAACAATGATGCCCTCTTCGRCCCGGATATGTGGCCCTATTTCGCATTAT	6480
BDV JCTC...C.....C.....G.....	6480
BDV BrieseT...T.....T.....A.....	6480
Consensus	CRAATGCGCATAYGGTYTAGCATTATAGATCATTTCAAAATTCCTACCGTTGTCTGCAAGTCAAGCTGTCCATATCGARGATG	6570
BDV JCTT...C.....G.....C.....A.....	6570
BDV BrieseC...T.....A.....T.....G.....	6570
Consensus	TTGCCCTAGAGAGTGTAGGTATAGGAATCTATCATYCAGGGTCTGTAGACACYACTGAGGGGTAYAACATGCAACCTTATTGGAG	6660
BDV JCTC.....C.....T.....C.....	6660
BDV BrieseT.....C.....C.....T.....	6660
Consensus	GTTCACCTTACCTTGCAGCCCAARCAAGYTAGCKAGGTTGACRTGGGGTGGAGACCTAGTTGGAGTYACAATGCCGTTTGTTCGCCAGCAAT	6750
BDV JCTG...C...G.....G.....T.....C.....	6750
BDV BrieseA...T...T.....A.....C.....	6750
Consensus	TCCATCCYCAAGTCTGTSGTGCAAAACRCRGAACCTCTACCTCGAYGCTATYATATACTGCCCCACARGAGACRTTGGCGTCACACCATC	6840
BDV JCTC...T.....C.....A...A.....T...C.....A...G.....	6840
BDV BrieseT...C.....G...G...G.....C...T.....G...A...A.....	6840
Consensus	TGACTACGAGGGGACGAGCGCTTTACCTYGGATCYAATACGGCTGTCCAMGGTYCAGCGAGGTGAGATCACRGGCCTAACAAAGTCAA	6930
BDV JCTT...T.....C...C.....C...T.....A.....G.....	6930
BDV BrieseC...C.....C...A...C.....G.....	6930
Consensus	GGGCTGCAATCTAGTCARGACACTCTCGTTCTCCAYCAGTGGTAYAARGTCCGTAARGTTACCGATCCACACTTGAACACYCTCATGG	7020
BDV JCTA.....A.....C.....C...G.....G.....T.....	7020
BDV BrieseG.....G.....T.....T...A.....A.....C.....	7020
Consensus	CRGCTTCTTCTTGTGAGAGGGRTACACATCTGACGCTCGRCCTAGCATYCAGGGTGGGACCTCACRCATCGTCTCCCATCCCGYGAG	7110
BDV JCT	.G.....G.....A.....A.....G.....T.....C.....A.....T.....	7110
BDV Briese	.A.....A.....G.....A.....C.....G.....G.....C.....	7110

FIG. 2J

Consensus	ACTCAGCGCARGGGTYACTGGGTATGTRAAATATACTMAGYACGTGGCTTCACAGTGATTATCTTCACACTCTTCTCGAAATCAT	7200
BDV JCTC.A.....C.....G.....C.C.....C.G.....	7200
BDV BrieseG.G.....T.....A.....A.T.....T.A.....	7200
Consensus	CAGAYGACTAYACAATCCACTTYCAGCATGTATTACACATACGGTTGCCCTATGCTGATTGGTGATTAGATCGGGCGGTATTATTC	7290
BDV JCTT.....C.....T.....	7290
BDV BrieseC.....T.....	7290
Consensus	CTCCTTACCTTTTGAGTGCAGTTGTAACATGCTTTGAGAAAGATAGACTCAGAGGAGKTCGCTGGCATGYGAACCYCAATAYAGGG	7380
BDV JCTT.....G.....G.....G.....C.....T.....T.....	7380
BDV BrieseT.....T.....T.....T.....C.....C.....	7380
Consensus	GTGCTGAGTGGCTGATATCAAGCCAGTYACTGTCCTGAGCAGATATGAYGCTGAAGTCGAGTTTGACCCCTGTGTGAGTGCGRGTT	7470
BDV JCTT.....T.....T.....C.....T.....	7470
BDV BrieseC.....C.....T.....C.....T.....G.....	7470
Consensus	ATTGCTCGGGATTCTCATTGGCAAGTCATTCTTTRGTTGACATTAAGGCAAGTGGGCATGATATATGAGCAGCGGACATGGGCTAAC	7560
BDV JCTG.....G.....G.....T.....T.....T.....	7560
BDV BrieseA.....A.....C.....C.....C.....	7560
Consensus	TGGAGAGGTTTCTGTRTCGGACATGCAGAAACTTCCTRTGGAGTATTGTAATTCGGTCTCTCTGGAGATTCCCTTATTGGCGCACGRCTCC	7650
BDV JCTG.....A.....A.....G.....A.....A.....	7650
BDV BrieseA.....A.....G.....G.....A.....G.....	7650
Consensus	TYCAGTTTCAGRAGGCTGGCTYATTAGRATGCTGCTATGCTGCRACAGGTCCCAACCCYTAGCTTCCCTAATGAAAGTYTTTCAAGACTCAG	7740
BDV JCTT.....G.....A.....A.....T.....T.....C.....	7740
BDV BrieseC.....C.....A.....G.....CC.....T.....T.....	7740
Consensus	CCCTMCTYATGGACTGGCACCCYCTYGTATGCTGGCTGTMCCTAGGATCAACTTTCATAGTCGGGGAGACCTCGTYGCTYAAAGCTYGTATTAT	7830
BDV JCTA.....T.....T.....T.....A.....C.....C.....C.....	7830
BDV BrieseC.....C.....C.....C.....C.....T.....T.....T.....	7830

FIG. 2K

Consensus	7920
BDV JCT	7920
BDV Briese	7920
TRCCCTTCATCAACCCGGGTATAGTGAGATTGAAGTGTCTTRGAATTAATAGCAAGTAYCATGCACTATCGGAGCCYAAATATGATCTGT .A.....A.....T.....T..... .G.....G.....C.....C.....	
Consensus	8010
BDV JCT	8010
BDV Briese	8010
ACATCGCTGCTGMAATCTGTGGGGTAAAGCCACACAGTTTGTGTGAGAAACAAACGACTTTACGGCCCGCCACCACCATGTTA.A.....A.....C.G.....G.....	
Consensus	8100
BDV JCT	8100
BDV Briese	8100
GTTATCCCTTCTTGGTCTAAGTCACGGCAATCAATCACAGGTCCTAAAGATGGTAGTRCGGAAGCTGAAGCTMTGTCTCTGTATATATA.....G.....A.....A.....A.....C.....	
Consensus	8190
BDV JCT	8190
BDV Briese	8190
ACCCCACAGTCGATCCCGCGGTTGCTCTCGACCTGTGCCAYCTGCCAGCACTAATACTAATATCTAGTCTGCGGGGTGACCCAGCGTACTC.G.....C.....T.A.....T.....	
Consensus	8280
BDV JCT	8280
BDV Briese	8280
AYGAGCGATTACTTGAGATGGACCTRTGCGGGGTGTCTCAAGTCGMYGATATCCCCCATTCYCTRGCTGSCAGAAGCGCAGGGGT .C.....A.....C.T.....C.A.....C..... .T.....G.....A.C.....T.G.....G.....	
Consensus	8370
BDV JCT	8370
BDV Briese	8370
TCCARTRGCCAGACGCTGTGTCAGGTGTRATTAGACTYGACARGTTAGAGTCRGTTTGTAYGCYACCCCTGTTTRGAGGARCTAG .A.A.A.....G.....T.....G.....C.C.....G..... ..G.G.G.....A.....C.....G.....T.T.....A.....A.....	
Consensus	8460
BDV JCT	8460
BDV Briese	8460
AGTTTATGCRATYCTAGACTCTGAGTTRGTTGAYATTAGTGATATGTGCTCCCTCCCTAGCAGACCCCTGTAAGCCCTTWTTCAGGCG.C.....A.....T.....C.....A.T.....G.....C.....T.....	
Consensus	8550
BDV JCT	8550
BDV Briese	8550
CARTRTATCGGAGCTTACAGTCGTTACAGTTAGCCTTAATGGACAACACTATAGTTTGTMTATGGACCTCATTAATGATCCGGRGRTGGACA ..G.G.....A.....C.....G..GG..... ..A.A.....C.....T.....A..AC.....	

FIG. 2L

Consensus	8640
BDV JCT	8640
BDV Briese	8640
	TYAGCCTCACCTGAGGARTTTGAYGARTGCTTGTGTGGTGGRCAGCAGAYATCCTCGGYCAGCCCGTCCCTAGTRGAGGTTGTTTACTACG .C.....G.....T.A.....G.G.....T.....T.....G..... .T.....A.....C.G.....A.A.....C.....C.....A.....
Consensus	8730
BDV JCT	8730
BDV Briese	8730
	TTGGAGTTGTRGGAAGCGYCCTGTGTTAGCGAGGCATCCSTGGTCAGCAGATCTTAAGCGAATYACTGTRGGGGGGCGRCKCCCTGCCG.....T.....C.....C.....A.....A.G.....A.....C.....G.....T.....G.....G.T.....
Consensus	8820
BDV JCT	8820
BDV Briese	8820
	CYTCTGCTGCGYRGAYTGGGTGATGAGGATTGTCRGGGGTCTCTGTGTGGTGGGCTTCCTGCTGGRTTGACGCAGTTRTGTGTRRTTGATT .T.....TG.C.....G.....C.....A.....C.....G.....G.GG..... .C.....CA.T.....A.....T.....T.....G.....A.....A.AA.....
Consensus	8910
BDV JCT	8908
BDV Briese	8910
	RAGRTYRAGCCAYCTACTRCCCTATTCTTAAAAAACCATAYGTCAGTGTGCTTGGGYTTGGTTGCTTTGTTGTAGCGCKTT G..G.TG....T...G.....C.....T.....T.....T-- A..A.CA....C....A.....T.....C.....G.....

FIG. 2M

FIG 3A

FIG 3B

C H1 H2 H3 M (bp)



	10	20	30	40	50	60	70	80	90	100	
Strain V	ATGGCAACCGCACCATTGAGTCTGGTCTGACTCCCTGGAGGACGAGAAAGATCCCCAGACACTACGACGGGAACGACCCGGGGTCA	CCCAAGG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	100
H1	ATGGCAACCGCACCATTGAGTCTGGTCTGACTCCCTGGAGGACGAGAAAGATCCCCAGACACTACGACGGGAACGACCCGGGGTCA	CCCAAGG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	100
H2	ATGGCAACCGCACCATTGAGTCTGGTCTGACTCCCTGGAGGACGAGAAAGATCCCCAGACACTACGACGGGAACGACCCGGGGTCA	CCCAAGG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	100
H3	ATGGCAACCGCACCATTGAGTCTGGTCTGACTCCCTGGAGGACGAGAAAGATCCCCAGACACTACGACGGGAACGACCCGGGGTCA	CCCAAGG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	100
C6BV	ATGGCAACCGCACCATTGAGTCTGGTCTGACTCCCTGGAGGACGAGAAAGATCCCCAGACACTACGACGGGAACGACCCGGGGTCA	CCCAAGG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	100
	110	120	130	140	150	160	170	180	190	200	
Strain V	TCCCAAGGAATGATTGACCCCAACCAAGTAGACCCAGCTCCTGAAGGACCTCAGGAAGACCCCTCCATGATCTCAGACCCAGACCCGGAACCCGGAAGGGA	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	200
H1	TCCCAAGGAATGATTGACCCCAACCAAGTAGACCCAGCTCCTGAAGGACCTCAGGAAGACCCCTCCATGATCTCAGACCCAGACCCGGAACCCGGAAGGGA	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	200
H2	TCCCAAGGAATGATTGACCCCAACCAAGTAGACCCAGCTCCTGAAGGACCTCAGGAAGACCCCTCCATGATCTCAGACCCAGACCCGGAACCCGGAAGGGA	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	200
H3	TCCCAAGGAATGATTGACCCCAACCAAGTAGACCCAGCTCCTGAAGGACCTCAGGAAGACCCCTCCATGATCTCAGACCCAGACCCGGAACCCGGAAGGGA	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	200
C6BV	TCCCAAGGAATGATTGACCCCAACCAAGTAGACCCAGCTCCTGAAGGACCTCAGGAAGACCCCTCCATGATCTCAGACCCAGACCCGGAACCCGGAAGGGA	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	200
	210	220	230	240	250	260	270	280	290	300	
Strain V	GCAGCTGTGGAATGATGACTAATCAAGAAGTTAGTGACGGAGCTGGCCGAGAAATAGCATGATCGAGGCTGAGGAGGTGCGGGGCACTCTTTGGAGACATC	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	300
H1	GCAGCTGTGGAATGATGACTAATCAAGAAGTTAGTGACGGAGCTGGCCGAGAAATAGCATGATCGAGGCTGAGGAGGTGCGGGGCACTCTTTGGAGACATC	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	300
H2	GCAGCTGTGGAATGATGACTAATCAAGAAGTTAGTGACGGAGCTGGCCGAGAAATAGCATGATCGAGGCTGAGGAGGTGCGGGGCACTCTTTGGAGACATC	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	300
H3	GCAGCTGTGGAATGATGACTAATCAAGAAGTTAGTGACGGAGCTGGCCGAGAAATAGCATGATCGAGGCTGAGGAGGTGCGGGGCACTCTTTGGAGACATC	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	300
C6BV	GCAGCTGTGGAATGATGACTAATCAAGAAGTTAGTGACGGAGCTGGCCGAGAAATAGCATGATCGAGGCTGAGGAGGTGCGGGGCACTCTTTGGAGACATC	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	300
	310	320	330	340	350	360	370	380	390	400	
Strain V	TCGGCTCGTATCGAGGCAAGGGTTTGAGTCCCTGTCCGGCCCTCCCAAGTGGAAACCATCCAGACAGCTCAGCGGTGGGATCACTCCGAGACAGCATCAGGATCC	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	400
H1	TCGGCTCGTATCGAGGCAAGGGTTTGAGTCCCTGTCCGGCCCTCCCAAGTGGAAACCATCCAGACAGCTCAGCGGTGGGATCACTCCGAGACAGCATCAGGATCC	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	400
H2	TCGGCTCGTATCGAGGCAAGGGTTTGAGTCCCTGTCCGGCCCTCCCAAGTGGAAACCATCCAGACAGCTCAGCGGTGGGATCACTCCGAGACAGCATCAGGATCC	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	400
H3	TCGGCTCGTATCGAGGCAAGGGTTTGAGTCCCTGTCCGGCCCTCCCAAGTGGAAACCATCCAGACAGCTCAGCGGTGGGATCACTCCGAGACAGCATCAGGATCC	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	400
C6BV	TCGGCTCGTATCGAGGCAAGGGTTTGAGTCCCTGTCCGGCCCTCCCAAGTGGAAACCATCCAGACAGCTCAGCGGTGGGATCACTCCGAGACAGCATCAGGATCC	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	ATG	400

FIG. 4A-I

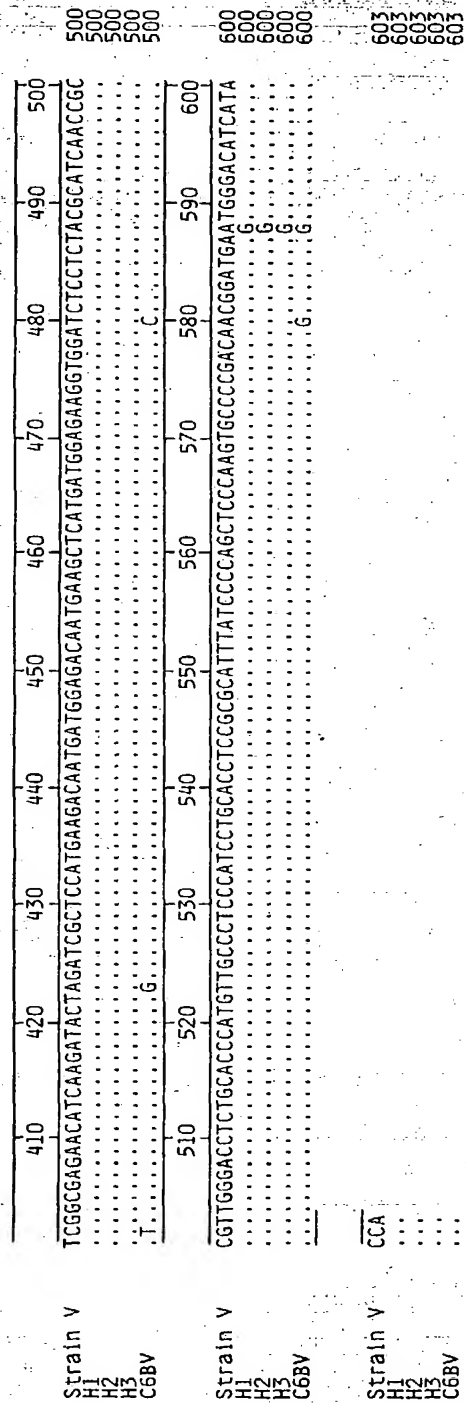


FIG. 4A-2

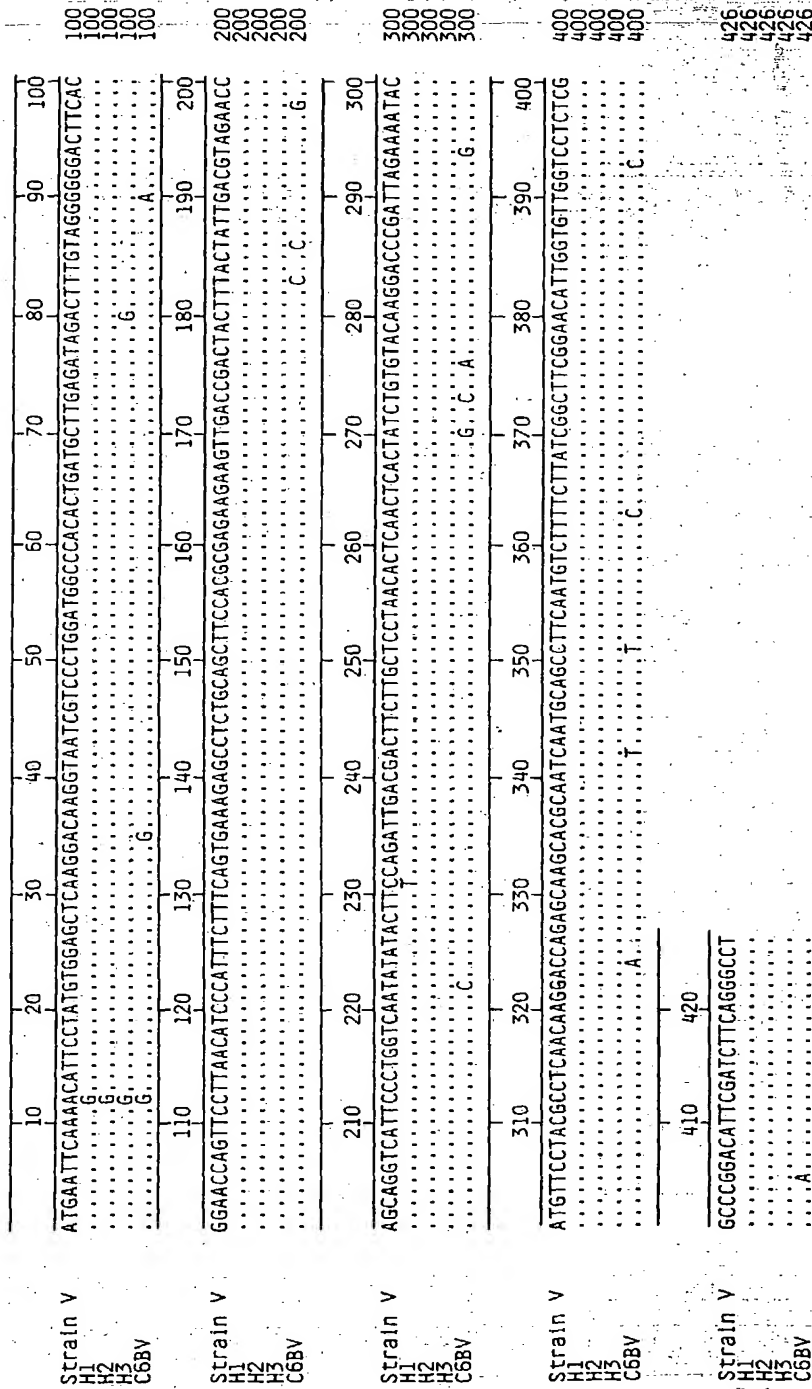
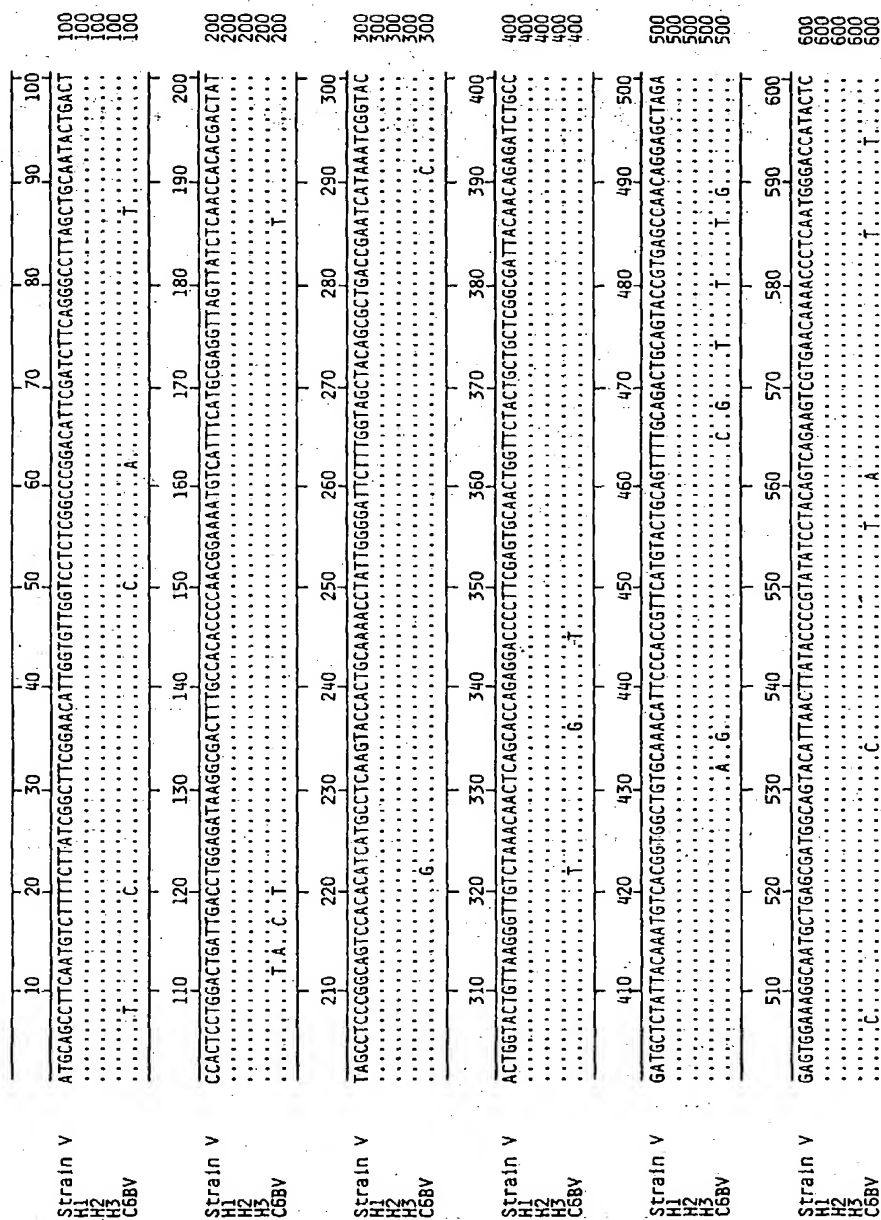


FIG. 4B



Strain V	610	620	630	640	650	660	670	680	690	700	700
H1	TGCACTCATCCTCTAAGATAGTTTCTTCGATGAATTTAGGGGTTTCATCTCCCTAAAGAAATGGTAGTTACCGAGGCTCATCAATGAGCGTGTG										700
H2										700
H3										700
C6BVC.....			G.....						700
Strain V	710	720	730	740	750	760	770	780	790	800	800
H1	CAAACTACACGTCGTCCTGCGGCCAGGTTGAAAAGGCGCGGTAGGAGACCCAGAGATTGAGTATCTAGTTTCAAGCTTAGGCCCACTGAAAGA										800
H2										800
H3										800
C6BV	T.....T.....T.....A.....G.....T.....T.....T.....A.....C.....C.....										800
Strain V	810	820	830	840	850	860	870	880	890	900	900
H1	TGCATGGGAGGACTGTGAGATCCTCCAGTCTCTGCTCCTAGGGGTGTTTGGTACTGGGATCGCAAGTGTCTTCAATTTTGAGGAGCTGGCTCAACAC										900
H2										900
H3										900
C6BVG.....T.....A.....A.....T.....T.....G.....C.....G.....										900
Strain V	910	920	930	940	950	960	970	980	990	1000	1000
H1	CCTGACATCATCGGGTATAGTTAATGGAGTTGGGGTTGTCTGGCAATGCCATCGTGTTAATGTACGTTTCATGCGGTGGAATGAGTCCACTATTACC										1000
H2										1000
H3										1000
C6BVT.....A.....A.....A.....A.....A.....A.....A.....A.....										1000
Strain V	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1100
H1	CTCCAGTAGATTACAATGGCGGGAAGTACTTCTGGAATGATGAGGGAAGGTTACACAAACACCCCGAGGCAAGGCCAGGGCTTAAGCGGGTCATGTG										1100
H2										1100
H3										1100
C6BVA.....T.....T.....G.....C.....C.....										1100
Strain V	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1200
H1	GTTGGCAGGTACTTCTTAGGGACAGTAGGGTCTGGGGTGAACCGAGGAGGATTCGGTACAAATAAGACCTCACATGACTACCACTGGAGGAGTTTGAG										1200
H2										1200
H3										1200
C6BVT.....T.....T.....T.....T.....T.....T.....T.....A.....										1200

FIG. 4C-2

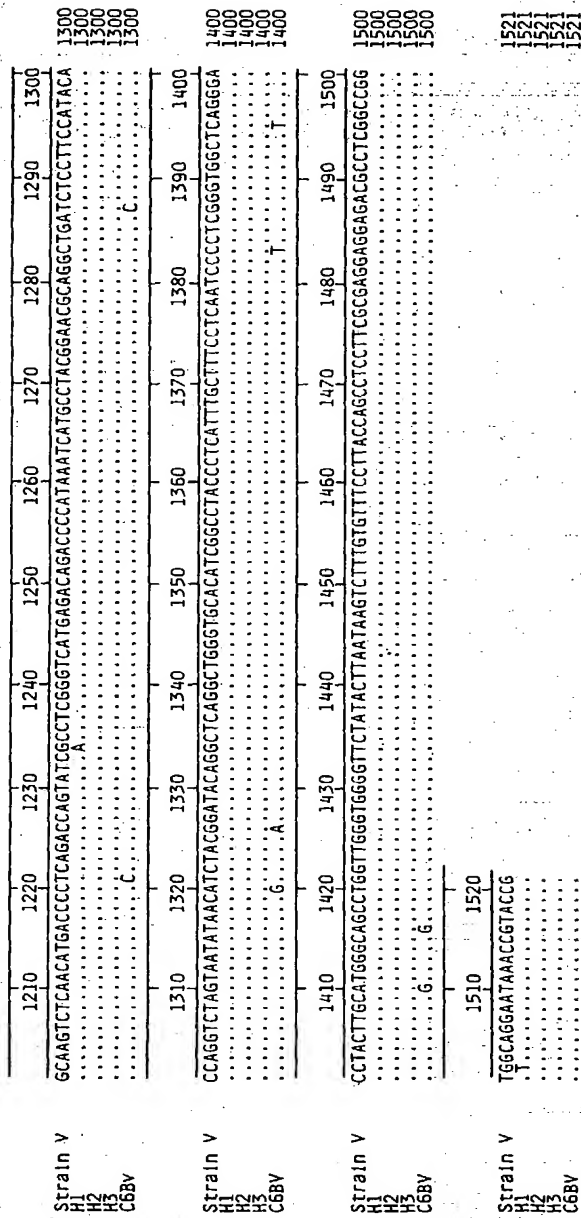


FIG. 4C-3

C6BV p40IntC.....	50
H1 p40IntC.....	50
H2 p40IntC.....	50
H3 p40IntC.....	50
StrainV p40IntT.....	50
Consensus	TTCAACAGT AACGCCAGC CTTGTGTTTCT ATGTTTGCT AATCCCAGGA	50
C6BV p40IntC.....	100
H1 p40IntC.....	100
H2 p40IntC.....	100
H3 p40IntC.....	100
StrainV p40IntC.....	100
Consensus	CTGCACGCTG CGTTTGTTCA CGGAGGGGTG CCTCGTGAAT GTACCTGTC	100
C6BV p40IntG.....	150
H1 p40IntG.....	150
H2 p40IntG.....	150
H3 p40IntG.....	150
StrainV p40IntG.....	150
Consensus	GACGCCTRTY ACGCGTGGRG AACAGACTGT YGTTAAGACT GORRAGTTTT	150
C6BV p40IntA.....	200
H1 p40IntA.....	200
H2 p40IntA.....	200
H3 p40IntA.....	200
StrainV p40IntA.....	200
Consensus	ACGGGGAAAA GACRACRAG CGTGATCTCA CCGAGCTGGA GATCTCCTCT	200
C6BV p40IntA.....	250
H1 p40IntA.....	250
H2 p40IntA.....	250
H3 p40IntA.....	250
StrainV p40IntA.....	250
Consensus	ATTTTCAGCC ATTGTTGCTC ATTACTAAATM GGGGTTGTGA TAGGATCGTC	250
C6BV p40IntT.....	300
H1 p40IntT.....	300
H2 p40IntT.....	300
H3 p40IntT.....	300
StrainV p40IntT.....	300
Consensus	RTCTAAGATY AAAGCAGTAG CCGAGCAGAT CAAGAAAAGG TTAAAACTA	300

FIG. 5A-1

FIG. 5A-2

Consensus	TGACCATGAG CTCAACGGG CTAACGAYC TTCTTAACCG GCTATCACAT	50
p180fragC.....C.....T.....	50
H1 p180T.....C.....	50
H2 p180T.....C.....	50
H3 p180T.....C.....	50
Strain 5 p180T.....C.....	50
Consensus	ACTATCACTA AGGGTGACTC CTTTGTATT AAQTMGAY ATAGTTCTG	100
p180fragT..A..T..C.....	100
H1 p180C..T..C.....	100
H2 p180C..T..C.....	100
H3 p180C..T..C.....	100
Strain 5 p180C..T..C.....	100
Consensus	GTGCAACGGT TTCCGACCAG AACTCARGC CCCATCTGT CGTCAGTTGG	150
p180fragA..A.....C.....	150
H1 p180G..G.....A.....	150
H2 p180G..G.....A.....	150
H3 p180G..G.....A.....	150
Strain 5 p180G..G.....A.....	150
Consensus	ATCAGATGTT CAATTGCGGG TACTTCTTCA GGACTGGGTG CACACTGCCA	200
p180frag	200
H1 p180	200
H2 p180	200
H3 p180	200
Strain 5 p180	200
Consensus	TGCTTTACCA CGTTTATTAT TCATGACAGR TTCAACCCGC CCTATTCCT	250
p180fragG.....A.....T.....	250
H1 p180A.....G.....C.....	250
H2 p180A.....G.....C.....	250
H3 p180A.....G.....C.....	250
Strain 5 p180A.....G.....C.....	250
Consensus	CTGTGGTGAG CCCGTTGAAG ACGGCTTAC ATGCGCGGTT GGGACTAATA	300
p180fragC.....T.....C.....G.....	300
H1 p180A.....A.....T.....A.....	300
H2 p180A.....A.....T.....A.....	300
H3 p180A.....A.....T.....A.....	300
Strain 5 p180A.....A.....T.....A.....	300

FIG. 5B-1

Consensus	CAATGGGGA GGGATGAGG CAGAACTAT GGACAATCT TACGAGCTGC	350
p180fragA.....T.....T.....	350
H1 p180G.....C.....C.....	350
H2 p180G.....C.....C.....	350
H3 p180G.....C.....C.....	350
Strain 5 p180G.....C.....C.....	350
Consensus	TGGGAGATAA TTGCTCTTCG GGAAATTAAC GTGACGTTA AATACTAGG	400
p180fragT.....	400
H1 p180C.....	400
H2 p180C.....	400
H3 p180C.....	400
Strain 5 p180C.....	400
Consensus	CCARGGTGAT AATCAGACAA TCATYRTACA TAAATCTGCA AGCCAAAATA	450
p180fragTG.....	450
H1 p180CA.....	450
H2 p180CA.....	450
H3 p180CA.....	450
Strain 5 p180CA.....	450
Consensus	ATCAGCTATT AGCGGAGCGA GCATIRGGG GYMTGTACAA GCATGCTAGA	500
p180fragT.....G.....A.....TT.....	500
H1 p180C.....C.....G.....CC.....	500
H2 p180C.....C.....G.....CC.....	500
H3 p180C.....C.....G.....CC.....	500
Strain 5 p180C.....C.....G.....CC.....	500
Consensus	TTAGCTGGCC ATAACCTYAA GGTAGARGAA TGMGGGTGT CAGATTGTCT	550
p180fragT.....A.....T.....	550
H1 p180C.....G.....C.....	550
H2 p180C.....G.....C.....	550
H3 p180C.....G.....C.....	550
Strain 5 p180C.....G.....C.....	550
Consensus	GTATGAGTAT GGAAAGAAGC TMTCTTCCG TGGTGTACCT GTCCCGGCT	600
p180fragC.....A.....	600
H1 p180T.....G.....	600
H2 p180T.....G.....	600
H3 p180T.....G.....	600
Strain 5 p180T.....G.....	600

FIG. 5B-2

Consensus	GTITGAAGCA GCTCTGCGG GTGACGGAT CACTGGGCA GTATTCCTCA	650.
p180fragG.....C.....G.....T.....	650
H1 p180A.....T.....A.....C.....	650
H2 p180A.....T.....A.....C.....	650
H3 p180A.....T.....A.....C.....	650
Strain 5 p180A.....T.....A.....C.....	650

Consensus	AACCTATACT CAAAGTTAGC CTGCTAACATCATORGY	689
p180fragT.....A.....C.....	689
H1 p180T.....A.....C.....	689
H2 p180T.....A.....C.....	689
H3 p180T.....A.....C.....	689
Strain 5 p180T.....A.....C.....	689

FIG. 5B-3

	p24					p16			p56														
	4	26	34	127	194	12	27	108	3	7	17	21	220	234	242	243	245	282	296	326	412	465	501
C6BV	G	S	I	H	A	G	D	E	L	S	A	Q	A	V	S	L	R	M	G	A	A	L	W
H1	E	-	V	Y	T	D	-	D	P	F	V	R	T	A	P	R	L	V	S	T	T	P	L
H2	-	-	V	-	T	-	-	D	P	F	V	R	T	A	P	R	L	V	S	T	-	P	-
H3	E	-	V	-	T	-	G	D	P	F	V	R	T	A	P	R	L	V	S	T	-	P	-
Strain V	R	P	V	-	T	D	-	D	P	F	V	R	T	A	P	R	L	V	S	-	-	P	-

FIG. 6A

	p24					p16					p56				
	C6BV	H1	H2	H3	Strain V	C6BV	H1	H2	H3	Strain V	C6BV	H1	H2	H3	Strain V
C6BV		16	14	14	17		17	16	17	16		67	65	65	64
H1	4		2	1	5	2		2	3	3	15		2	2	3
H2	2	2		2	3	1	1		1	1	13	2		0	1
H3	3	1	1		5	2	2	1		2	13	2	0		1
Strain V	4	3	2	2		1	1	0	1		12	3	1		1

FIG. 6B

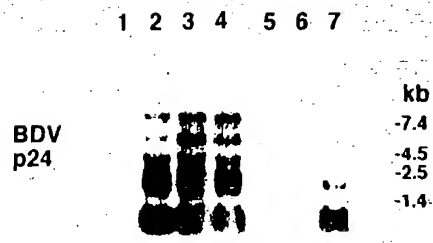


FIG. 7A

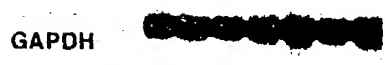


FIG. 7B

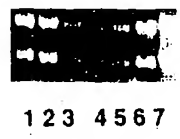


FIG. 7C

MATEPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPVRNALTPVDQLLKDLRKNPSMISDP
DQRTGREQLSNDELIKLVTELAENSMIEAEVVRGTLGDISARIEAGFESLSALQVETIQ
AQRCDSIRILGENIKILDRSMKTMETMKLMMEKVDLLYASTAVGTSAPMLPSHP
APPRYPQLPSAPTIDEWDIIP

FIG. 8A

MATGPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPVRNALTPVDQLLKDLRKNPSMISDP
DQRTGREQLSNDELIKLVTELAENSMIEAEVVRGTLGDISARIEAGFESLSALQVETIQ
AQRCDSIRILGENIKILDRSMKTMETMKLMMEKVDLLYASTAVGTSAPMLPSHP
APPRYPQLPSAPTIDEWDIIP

FIG. 8B

MATEPSSLVDSLEDEEDPQTLRRERSGSPRPRKVPVRNALTPVDQLLKDLRKNPSMISDP
DQRTGREQLSNDELIKLVTELAENSMIEAEVVRGTLGDISARIEAGFESLSALQVETIQ
AQRCDSIRILGENIKILDRSMKTMETMKLMMEKVDLLYASTAVGTSAPMLPSHP
APPRYPQLPSAPTIDEWDIIP

FIG. 8C

MNSKHSYVELKDKVIVPGWPTLMLEIDFVGGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLTLNLSVYKDPYKYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9A

MNSKHSYVELKDKVIVPGWPTLMLEIDFVGGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLTLNLSVYKDPYKYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9B

MNSKHSYVELKDKVIVPGWPTLMLEIGFVGGTSRNQFLNIPFLSVKEPLQLPREKKLTDY
FTIDVEPAGHSLVNIYFQIDDFLLTLNLSVYKDPYKYMFLRLNKDQSKHAINAAFNVF
SYRLRNIGVGPLGPDIRSSGP

FIG. 9C

MQPSMSFLIGFGLVLVLSARTFDLQGLSCNTDSTPGLIDLEIRRLCHTPTENVISCEVSYL
NHTTISLPAVHTSCLKYHCKTYWGFFGSYADRINRYTGTGCLNNSAPEDPPECNW
FYCCSAITTEICRCSTNVTVAQTFPPFMYCSFADCSYVSSQEELESGKAMLSDGSTLTYY
PYLQSEVNVNKTNGTILCNSSSKIVSDEFRRSYSLTNGSYQSSINVTANYTSSCRPRL
KRRRDTQQIEYL VHKLRPTLKDA WEDCEILQSLLGVFGTGIASQFLRSWLNHPDII
GYVNGVGWVWQCHRVNVTFTWNESTYYPVDYNGRKYFLNDEGRQLQNTPEARPG
LKRVMWFGRYFLGTGSGVKPRRIRYNKTSHDYHLEEFASLNMTPQTSITSGHETDPI
NHA YGTQADLLPYTRSSNITSTDTGSGWVHIGLPSF AFLNPLGWLRLDLLA WAAWLGGV
LYLISLCVSLPASFAARRRLGR LQE

FIG. 10A

MQPSMSFLIGFGLVLVLSARTFDLQGLSCNTDSTPGLIDLEIRRLCHTPTENVISCEVSYL
NHTTISLPAVHTSCLKYHCKTYWGFFGSYADRINRYTGTGCLNNSAPEDPPECNW
FYCCSAITTEICRCSTNVTVAQTFPPFMYCSFADCSYVSSQEELESGKAMLSDGSTLTYY
PYLQSEVNVNKTNGTILCNSSSKIVSDEFRRSYSLTNGSYQSSINVTANYTSSCRPRL
KRRRDTQQIEYL VHKLRPTLKDA WEDCEILQSLLGVFGTGIASQFLRSWLNHPDII
GYVNGVGWVWQCHRVNVTFTWNESTYYPVDYNGRKYFLNDEGRQLQNTPEARPG
LKRVMWFGRYFLGTGSGVKPRRIRYNKTSHDYHLEEFASLNMTPQTSITSGHETDPI
NHA YGTQADLLPYTRSSNITSTDTGSGWVHIGLPSF AFLNPLGWLRLDLLA WAAWLGGV
LYLISLCVSLPASFAARRRLGR WQE

FIG. 10B

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTSLVFL	CLLIRGLHAA	FVHGGVPRES	YLSPTVRGE	QIVWKTAEFY
50				
GEKITQDILT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAGA	EQIKRRFKTM
100				
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGGSFVLS	LLTTDFESPG
150				
KERMQIKLV	ASYAQMTTYT	TIKEYLAECM	DATLTIPFW	
189				

FIG. IIA

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTSLVFL	CLLIRGLHAA	FVHGGVPRES	YLSPTVRGE	QIVWKTAEFY
50				
GEKITQDILT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAGA	EQIKRRFKTM
100				
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGGSFVLS	LLTTDFESPG
150				
KERMQIKLV	ASYAQMTTYT	TIKEYLAECM	DATLTIPFW	
189				

FIG. IIB

10	20	30	40	50
1234567890	1234567890	1234567890	1234567890	1234567890
HIVTSLVFL	CLLIRGLHAA	FVHGGVPRES	YLSPTVRGE	QIVWKTAEFY
50				
GEKITQDILT	ELEISSIFSH	CCSLLIGWVI	GSSSKIKAGA	EQIKRRFKTM
100				
MAALNRPSHG	ETATLLQMFN	PHEAIDWING	QFWGGSFVLS	LLTTDFESPG
150				
KERMQIKLV	ASYAQMTTYT	TIKEYLAECM	DATLTIPFW	
189				

FIG. IIC

10	20	30	40	50	
1234567890	1234567890	1234567890	1234567890	1234567890	
TMSSTALTHL	LNRLSHITIK	GDSFVINLDY	SSWNGFRPE	LQAPICRQID	50
QMFNGYFFR	TGCTLPCTT	FIIQDRFNPP	YSLSGEPVED	GVTCVVGIRT	100
MGEQMRQKLW	TILTSCWEII	ALREINVTFN	ILOGGDNQTI	IIHKSASQNN	150
QLLAERALGA	LYKHARLAGH	NLKVEECWVS	DCLYEYGGKL	FFRGVFPVGC	200
LKQLSRVIDS	TGELFPNLVS	KLACLTSSC			229

FIG. 12